

M. Ibrahim

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/435,054

DATE: 08/07/2001
TIME: 08:22:55

Input Set : A:\0943SEQLIST.txt
Output Set: N:\CRF3\08072001\I435054.raw

PS

4 <110> APPLICANT: Lowe, Keith S.
5 Gordon-Kamm, William J.
6 Klein, Theodore M.
7 Rasco-Gaunt, Sonriza
8 Cahoon, Rebecca E.
9 Sun, Xifan
10 Hoester, George J.
11 Gregory, Carolyn A.
12 Nadimpalli, Ramgopal
14 <120> TITLE OF INVENTION: Transcriptional Activator Nucleic Acids,
15 Polypeptides, and Methods of Use Thereof
18 <130> FILE REFERENCE: 0943
20 <140> CURRENT APPLICATION NUMBER: 09/435,054
21 <141> CURRENT FILING DATE: 1999-11-08
23 <150> PRIOR APPLICATION NUMBER: 60/107,643
24 <151> PRIOR FILING DATE: 1998-11-09
26 <160> NUMBER OF SEQ ID NOS: 23
28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 1173
32 <212> TYPE: DNA
33 <213> ORGANISM: Zea mays
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (69)...(902)
39 <400> SEQUENCE: 1
40 ccacgcgtcc gccaccacac cacgagcgcg cgataaccct agcttagcttc aggttagtagc 60
41 gagagcca atg gac tcc agc agc ttc ctc cct gcc gcc ggc ggc gag aat 110
42 Met Asp Ser Ser Ser Phe Leu Pro Ala Ala Gly Ala Glu Asn
43 1 5 10
45 ggc tcg gcg ggc ggc gcc aac aat ggc ggc gct gct cag cag cat 158
46 Gly Ser Ala Ala Gly Gly Ala Asn Asn Gly Gly Ala Ala Gln Gln His
47 15 20 25 30
49 gcg gcg ccg gcg atc cgc gag cag gac cgg ctg atg ccg atc gcg aac 206
50 Ala Ala Pro Ala Ile Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn
51 35 40 45
53 gtg atc cgc atc atg cgg cgc gtg ctg ccg gcg cac gcc aag atc tcg 254
54 Val Ile Arg Ile Met Arg Arg Val Leu Pro Ala His Ala Lys Ile Ser
55 50 55 60
57 gac gac gcc aag gag acg atc cag gag tgc gtg tcg gag tac atc agc 302
58 Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser
59 65 70 75
61 ttc atc acg ggg gag gcc aac gag cgg tgc cag cgg gag cag cgc aag 350
62 Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys
63 80 85 90
65 acc atc acc gcc gag gac gtg ctg tgg gcc atg agc cgc ctc ggc ttc 398
66 Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser Arg Leu Gly Phe

ENTERED

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67	95	100	105	110													
69	gac	gac	tac	gtc	gag	ccg	ctc	ggc	gcc	tac	ctc	cac	cgc	tac	cgc	gag	446
70	Asp	Asp	Tyr	Val	Glu	Pro	Leu	Gly	Ala	Tyr	Leu	His	Arg	Tyr	Arg	Glu	
71																115	
73	ttc	gag	ggc	gac	gcg	cgc	ggc	gtc	ggg	ctc	gtc	ccg	ggg	gcc	gcc	cca	494
74	Phe	Glu	Gly	Asp	Ala	Arg	Gly	Val	Gly	Leu	Val	Pro	Gly	Ala	Ala	Pro	
75																130	
77	tcg	cgc	ggc	gac	cac	cac	ccg	cac	tcc	atg	tcg	cca	gcg	gcg	atg	542	
78	Ser	Arg	Gly	Gly	Asp	His	His	Pro	His	Ser	Met	Ser	Pro	Ala	Ala	Met	
79																145	
81	ctc	aag	tcc	cgc	ggg	cca	gtc	tcc	gga	gcc	atg	cta	ccg	cac	cac	590	
82	Leu	Lys	Ser	Arg	Gly	Pro	Val	Ser	Gly	Ala	Ala	Met	Leu	Pro	His	His	
83																160	
85	cac	cac	cac	cac	gac	atg	cag	atg	cac	gcc	atg	tac	ggg	gga	acg	638	
86	His	His	His	His	Asp	Met	Gln	Met	His	Ala	Ala	Met	Tyr	Gly	Gly	Thr	
87																175	
89	gcc	gtg	ccc	ccg	ccg	gcc	ggg	cct	cct	cac	cac	ggc	ggg	ttc	ctc	atg	686
90	Ala	Val	Pro	Pro	Pro	Ala	Gly	Pro	Pro	His	His	Gly	Gly	Phe	Leu	Met	
91																195	
93	cca	cac	cca	cag	ggt	agt	agt	agc	cac	tac	ctg	cct	tac	gag	ccc	734	
94	Pro	His	Pro	Gln	Gly	Ser	Ser	His	Tyr	Leu	Pro	Tyr	Ala	Tyr	Glu	Pro	
95																210	
97	acg	tac	ggc	ggt	gag	cac	gcc	atg	gct	gca	tac	tat	gga	ggc	gcc	782	
98	Thr	Tyr	Gly	Gly	Glu	His	Ala	Met	Ala	Ala	Tyr	Tyr	Gly	Gly	Ala	Ala	
99																225	
101	tac	gac	ccc	ggc	aac	ggc	ggg	agc	ggc	gac	ggc	agt	ggc	agt	ggc	830	
102	Tyr	Ala	Pro	Gly	Asn	Gly	Gly	Ser	Gly	Asp	Gly	Ser	Gly	Ser	Gly		
103																240	
105	ggt	ggc	ggg	agc	gac	tac	aca	ccg	cag	ggc	agc	ggc	ggc	ttg	gag	878	
106	Gly	Gly	Gly	Ser	Ala	Ser	His	Thr	Pro	Gln	Gly	Ser	Gly	Gly	Leu	Glu	
107																255	
109	cac	ccg	cac	ccg	tcc	gac	tac	aag	tagctagttc	gtacgtcggt	cgacttgagc					932	
110	His	Pro	His	Pro	Phe	Ala	Tyr	Lys									
111																275	
113	aagccatgca	tctgctgatc	tgaacgtacg	ctgtattgt	cacgcacgca	cgtacgtatc										992	
114	ggcggctagc	tctcctgttt	aagttgtact	gtgattctgt	cccgccggc	tagcaactta										1052	
115	gtatcttct	tcagtctcta	gtttcttagc	agtcgttagaa	gtgttcaatg	cttgcagg										1112	
116	tgttgtttta	gggcgggggt	aaaccatccg	atgagattat	ttcaaaaaaa	aaaaaaaaaa										1172	
117	a															1173	
119	<210>	SEQ ID NO:	2														
120	<211>	LENGTH:	278														
121	<212>	TYPE:	PRT														
122	<213>	ORGANISM:	Zea mays														
124	<400>	SEQUENCE:	2														
125	Met	Asp	Ser	Ser	Ser	Phe	Leu	Pro	Ala	Ala	Gly	Ala	Glu	Asn	Gly	Ser	
126	1					5					10					15	
127	Ala	Ala	Gly	Gly	Ala	Asn	Asn	Gly	Gly	Ala	Ala	Gln	Gln	His	Ala	Ala	
128																20	
129	Pro	Ala	Ile	Arg	Glu	Gln	Asp	Arg	Leu	Met	Pro	Ile	Ala	Asn	Val	Ile	
																25	
																30	

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130	35	40	45
131	Arg Ile Met Arg Arg Val Leu Pro Ala His Ala Lys Ile Ser Asp Asp		
132	50	55	60
133	Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile		
134	65	70	75
135	80		
136	Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile		
137	85	90	95
138	Thr Ala Glu Asp Val Leu Trp Ala Met Ser Arg Leu Gly Phe Asp Asp		
139	100	105	110
140	Tyr Val Glu Pro Leu Gly Ala Tyr Leu His Arg Tyr Arg Glu Phe Glu		
141	115	120	125
142	Gly Asp Ala Arg Gly Val Gly Leu Val Pro Gly Ala Ala Pro Ser Arg		
143	130	135	140
144	Gly Gly Asp His His Pro His Ser Met Ser Pro Ala Ala Met Leu Lys		
145	145	150	155
146	160		
147	Ser Arg Gly Pro Val Ser Gly Ala Ala Met Leu Pro His His His		
148	165	170	175
149	His His Asp Met Gln Met His Ala Ala Met Tyr Gly Gly Thr Ala Val		
150	180	185	190
151	Pro Pro Pro Ala Gly Pro Pro His His Gly Gly Phe Leu Met Pro His		
152	195	200	205
153	Pro Gln Gly Ser Ser His Tyr Leu Pro Tyr Ala Tyr Glu Pro Thr Tyr		
154	210	215	220
155	Gly Gly Glu His Ala Met Ala Ala Tyr Tyr Gly Ala Ala Tyr Ala		
156	225	230	235
157	240		
158	Pro Gly Asn Gly Gly Ser Gly Asp Gly Ser Gly Ser Gly Gly Gly		
159	245	250	255
160	Gly Ser Ala Ser His Thr Pro Gln Gly Ser Gly Gly Leu Glu His Pro		
161	260	265	270
162	His Pro Phe Ala Tyr Lys		
163	275		
164	<210> SEQ ID NO: 3		
165	<211> LENGTH: 20		
166	<212> TYPE: DNA		
167	<213> ORGANISM: Artificial Sequence		
168	<220> FEATURE:		
169	<223> OTHER INFORMATION: primer		
170	<400> SEQUENCE: 3		
171	tagtagcgag agccaatgga	20	
172	<210> SEQ ID NO: 4		
173	<211> LENGTH: 20		
174	<212> TYPE: DNA		
175	<213> ORGANISM: Artificial Sequence		
176	<220> FEATURE:		
177	<223> OTHER INFORMATION: primer		
178	<400> SEQUENCE: 4		
179	gccgggacag aatcacagta	20	
180	<210> SEQ ID NO: 5		
181	<211> LENGTH: 20		

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Input Set : A:\0943SEQLIST.txt
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186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: primer
192 <400> SEQUENCE: 5
193 tagtagcgag agccaatgga 20
195 <210> SEQ ID NO: 6
196 <211> LENGTH: 20
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
200 <220> FEATURE:
201 <223> OTHER INFORMATION: primer
203 <400> SEQUENCE: 6
204 cccggcccta aaacaacaca 20
206 <210> SEQ ID NO: 7
207 <211> LENGTH: 481
208 <212> TYPE: DNA
209 <213> ORGANISM: Argemone mexicana
211 <220> FEATURE:
212 <221> NAME/KEY: CDS
213 <222> LOCATION: (44)...(481)
215 <221> NAME/KEY: misc_feature
216 <222> LOCATION: (1)...(481)
217 <223> OTHER INFORMATION: n = A,T,C or G
219 <400> SEQUENCE: 7
220 cgagagaaaag agtttgtgaa gaagaagaag aagttgaaaa gag atg gaa cgt ggt 55
221 Met Glu Arg Gly
222 1
224 ggt ggt ggt ggt agt ggt ggt ttc cat gga tat cag aaa ctc 103
225 Gly Gly Gly Gly Ser Gly Gly Phe His Gly Tyr Gln Lys Leu
226 5 10 15 20
228 cca aaa tca aac tcc gct gga atg atg ctc tcg gag cta tcg aat aac 151
229 Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu Leu Ser Asn Asn
230 25 30 35
232 aac aac aat att gac gta aac tct aca tgt act gta cga gag caa gat 199
233 Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val Arg Glu Gln Asp
234 40 45 50
236 cga tac atg cca att gct aat gtg atc agg atc atg cgt aag gta ctt 247
237 Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Val Leu
238 55 60 65
240 cct act cat gcc aag atc tct gac gat gcc aaa gaa act atc caa gaa 295
241 Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu
242 70 75 80
244 tgt gtc tca gaa tac atc agt ttc atc aca agt gaa gcc aat gat cgt 343
245 Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu Ala Asn Asp Arg
246 85 90 95 100
248 tgc caa cgt gaa caa aga aag aca atc aca gct gaa gat gtt tta tgg 391
249 Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp
250 105 110 115

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W--> 252 gcg atg agc aaa cta ggg ntt gat gag tac att gaa cct cta act ctt 439
 W--> 253 Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu Pro Leu Thr Leu
 254 120 125 130
 W--> 256 tac ctt caa cgt tat cgt gag ttt gaa ggt gna cgt tgg tca
 W--> 257 Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg Trp Ser 481
 258 135 140 145
 261 <210> SEQ ID NO: 8
 262 <211> LENGTH: 146
 263 <212> TYPE: PRT
 264 <213> ORGANISM: Argemone mexicana
 266 <220> FEATURE:
 267 <221> NAME/KEY: VARIANT
 268 <222> LOCATION: (1)...(146)
 269 <223> OTHER INFORMATION: Xaa = Any Amino Acid
 271 <400> SEQUENCE: 8
 272 Met Glu Arg Gly Gly Gly Gly Ser Gly Gly Gly Phe His Gly
 273 1 5 10 15
 274 Tyr Gln Lys Leu Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu
 275 20 25 30
 276 Leu Ser Asn Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val
 277 35 40 45
 278 Arg Glu Gln Asp Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met
 279 50 55 60
 280 Arg Lys Val Leu Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu
 281 65 70 75 80
 282 Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu
 283 85 90 95
 284 Ala Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu
 285 100 105 110
 286 Asp Val Leu Trp Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu 47
 287 115 120 125
 288 Pro Leu Thr Leu Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg
 289 130 135 140
 290 Trp Ser
 291 145
 293 <210> SEQ ID NO: 9
 294 <211> LENGTH: 942
 295 <212> TYPE: DNA
 296 <213> ORGANISM: Glycine max
 298 <220> FEATURE:
 299 <221> NAME/KEY: CDS
 300 <222> LOCATION: (3)...(722)
 302 <400> SEQUENCE: 9
 303 gc acg agc tct ctt ata atc aca cac aca cct acc tta ata gct atg
 304 Thr Ser Ser Leu Ile Ile Thr His Thr Pro Thr Leu Ile Ala Met 47
 305 1 5 10 15
 307 gaa act gga ggc ttt cac ggc tac cgc aag ctc ccc aac acc acc gct
 308 Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr Ala 95
 309 20 25 30

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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DATE: 08/07/2001
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L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:694 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:702 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23